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shown over and under the exonic structure (arrowheads). Exon-intron boundaries of exons 9, 10, 11 and 17 are shown in the upper part of the diagram (uppercase = exon, lowercase = intron), and the region covered by the two PAC clones is illustrated by the two lines at the bottom of the figure. The approximate location of the sequence polymorphisms, discovered in the families with severe hyperglycerolemia, are indicated by the arrows. The polymorphic base and surrounding sequence appear beneath the arrows (SEQ ID NOS: 20-23).

REMARKS

The amendment to the Specification identifies the SEQ ID NOS of the corresponding four polynucleotide sequences disclosed in Figure 2. No new matter has been added.

Respectfully submitted,

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MARKED UP VERSION OF AMENDMENTSSpecification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace the paragraph at page 5, lines 1 through 22 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

Figure 2 shows the exonic structure of the Xp GK gene and location of sequence polymorphisms. The first PAC clone, RPCI-5.931_C_24, containing exons 1 to 12 was used as sequencing template for exons 9, 10 and 11. An insert of 394 base pairs (bp) was found after the 36th nucleotide of exon 9, suggesting that the originally described exon actually consists of two exons (9A and 9B). These exons are 36 and 68 bases in length, respectively, and the corresponding intron-exon boundaries have the expected consensus splice site sequence as shown. When the sequence obtained for intron 10 was aligned with the published cDNA sequence, it was discovered that the splice junctions had been incorrectly defined, so that the last 12 bases of exon 10 were in fact encoded by exon 11. Furthermore, when the entire intron was sequenced, rather than being greater than 8 kilobases (kb) in length as originally believed, it was found to be 456 bp. Using primers located in introns 16 and 18 (forward and reverse primers, respectively), an amplicon was generated from the second clone, RPCI-5.1150_E_8 and then sequenced to determine the sequence of the 3' end of intron 7. Boxes show each exon and its length in base pairs (intron length not drawn to scale). Primers used to amplify each exon are shown over and under the exonic structure (arrowheads). Exon-intron boundaries of exons 9, 10, 11 and 17 are shown in the upper part of the diagram (uppercase = exon, lowercase = intron), and the region covered by the two PAC clones is illustrated by the two lines at the bottom of the figure. The approximate location of the sequence polymorphisms, discovered in the families with severe hyperglycerolemia, are indicated by the arrows. The polymorphic base and surrounding sequence appear beneath the arrows (SEQ ID NOS: 20-23).